

- (B) amplifying DNA of said target human containing each of said polymorphic sites;
- (C) determining the identity of the single nucleotide present at each of said single nucleotide polymorphic sites; and
- (D) comparing the identity of said determined single nucleotide present at each of said single nucleotide polymorphic sites with the identity of a reference nucleotide, said reference nucleotide being present at each of said single nucleotide polymorphic sites in a reference [organism] human.

[Please amend claim 48 as follows:]

48 [Amended]. The method of claim 47, wherein said method additionally comprises identifying the presence of a genetic trait of said target human, and wherein at least one of said single nucleotide polymorphic sites **[is within about 150 bases of said genetic trait] segregates non-randomly with respect to said genetic trait and is predictive of the probability that said target human exhibits said trait.**

[Please amend claim 49 as follows:]

49 [Amended]. A method for determining whether a target human possesses a genetic trait, said method comprising the steps:

- (A) amplifying a DNA molecule of said human, wherein said DNA molecule contains at least one single nucleotide polymorphism and wherein said single nucleotide polymorphism **[is within about 150 bases of said genetic trait] segregates non-randomly with said genetic trait and is predictive of the probability that said target human exhibits said trait;**
- (B) incubating the DNA of said human in the presence of a nucleic acid primer and from one to four dideoxynucleotide derivatives, under conditions sufficient to permit a polymerase mediated, template-dependent extension of said primer, said extension causing the incorporation of a single dideoxynucleotide derivative to the 3'-terminus of said primer, said incorporated single dideoxynucleotide derivative being complementary to the single nucleotide of the polymorphic site of said polymorphism;
- (C) determining the identity of said single nucleotide of said single nucleotide polymorphism by determining the identity of the dideoxynucleotide derivative incorporated into said primer, said identified dideoxynucleotide derivative being complementary to said single nucleotide of said polymorphism;
- (D) comparing the identity of said single nucleotide of said single nucleotide polymorphism with a corresponding single nucleotide polymorphism of a

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- (E) reference human, and determining whether said single nucleotide polymorphisms contain the same single nucleotide at their respective polymorphic sites; and using said comparison to determine whether said target human possesses said genetic trait. --

Please add the following new claims:

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- 51. A method for analyzing nucleic acid of a target human by identifying the nucleotide present at at least two preselected single nucleotide polymorphic sites, wherein said method comprises:
- (A) selecting said single nucleotide polymorphic sites for such analysis;
 - (B) hybridizing at least two primer molecules to at least one nucleic acid molecule of said target human, wherein one of said primer molecules specifically hybridizes to an invariant proximal nucleotide sequence or an invariant distal nucleotide sequence of one of said single nucleotide polymorphic sites and another of said primer molecules specifically hybridizes to another invariant proximal nucleotide sequence or invariant distal nucleotide sequence of one of said single nucleotide polymorphic sites;
 - (C) determining the identity of the nucleotide present at each of said selected single nucleotide polymorphic sites; and
 - (D) comparing the identity of said determined nucleotide present at each of said single nucleotide polymorphic sites with the identity of a reference nucleotide, said reference nucleotide being present at each of said single nucleotide polymorphic sites in a reference organism.
52. The method according to claim 48, wherein at least one of said single nucleotide polymorphisms is within 150 bases of said genetic trait.
53. The method according to claim 49, wherein at least one of said single nucleotide polymorphisms is within 150 bases of said genetic trait.--

REMARKS

I. Status of the Application

Claims 34-38, 42-44 and 47-50 were pending, and new claims 51-53 has been added. Therefore, claims 34-38, 42-44, 47-50 and 51-53 are pending.